

30.APR.2002 18:07

O BIOCHEMISTRY 643 479 7866

esday, 30 April 2002

O U BIOCHEMISTRY



# results of BLAST

TBLASTN 2.2.3 [Apr-24-2002]

## References:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

RID: 1020140625-011436-28352

## Query:

(324 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)  
1,218,445 sequences; 5,427,962,278 total letters

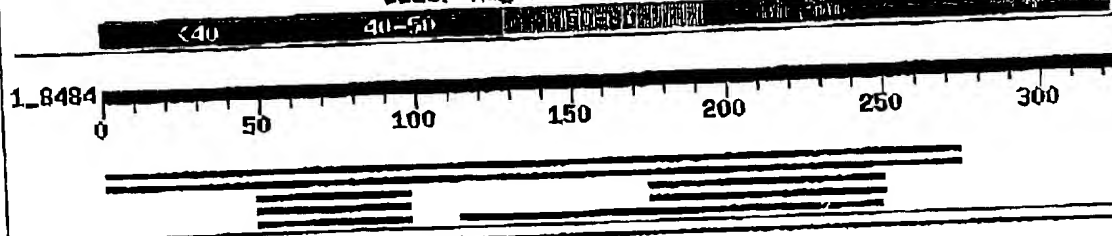
If you have any problems or questions with the results of this search please refer to the [BLAST FAQ](#)

## Taxonomy reports

## Distribution of 9 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignment

### Color Key for Alignment Scores



## Sequences producing significant alignments:

Score E  
(bits) Value

gi 2636718 gb AF007776.1 AF007776	Candida albicans	549	e-154
gi 3273716 gb AF050216.1 AF050216	Candida albicans chromoso...	549	e-154
gi 13366236 gb U22831.2	Caenorhabditis elegans cosmid F47D...	40	0.30
gi 17553483 ref NM_065980.1	Caenorhabditis elegans	40	0.30
gi 20197177 gb AC005397.3	Arabidopsis thaliana chromosome ...	32	4.1
gi 1754514 gb D87515.1 D87515	Rattus norvegicus mRNA for a...	35	9.7
gi 13592046 ref NM_031097.1	Rattus norvegicus aminopeptida...	35	9.7
gi 2039142 gb U61696.1 RN061696	Rattus norvegicus aminopept...	35	9.7

## Alignments

>gi|2636718|gb|AF007776.1|AF007776 Candida albicans  
Length = 6426

Score = 549 bits (1615), Expect = e-154  
Identities = 272/274 (99%). Positives = 272/274 (99%)  
Frame = +2

Query: 1 MSSAKNDNDEGKVMESVDQANAIKVDHRIKARFNMLFIKFNLDLPKLAVGNQKSVQKWN 60  
MSSAKNDNDEGKVMESVDQANAIKVDHRIKARFNMLFIKFNLDLPKLAVGNQKSVQKWN 577  
Sbjct: 398 MSSAKNDNDEGKVMESVDQANAIKVDHRIKARFNMLFIKFNLDLPKLAVGNQKSVQKWN 577

Query: 61 EFKYPHVAYPDVLEFLLDYNNPKDKFKVKKVVEGIYPTGWCLQMCLOSIQFDRFRLLIMISKLE 120  
EFKYPHVAYPDVLEFLLDYNNPKDKFKVKKVVEGIYPTGWCLQMCLOSIQFDRFRLLIMISKLE 757  
Sbjct: 578 EFKYPHVAYPDVLEFLLDYNNPKDKFKVKKVVEGIYPTGWCLQMCLOSIQFDRFRLLIMISKLE 757

Query: 121 KHLQKEANLIKAAYDAVTKSKDYTTISKILSKFVNVEHELVCYNLPYLSQVEEKLEIL 180  
KHLQKEANLIKAAYDAVTKSKDYTTISKIL KFNVEHELVCYNLPYLSQVEEKLEIL  
Sbjct: 758 KHLQKEANLIKAAYDAVTKSKDYTTISKILKFNVEHELVCYNLPYLSQVEEKLEIL 937

Query: 181 YNTSNVDEYVRSPLNLIGQVLYFNHVKKSEALSLFLNIHASYYSKWIQADNDTSVLPSC 240  
YNTSNVDEYVRSPLNLIGQVLYFNHVKKSEALSLFLNIHASYYSKWIQADNDTSVLPSC

Received Time 30.Apr. 18:38 <http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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O U BIOCHEMISTRY ryskwIQADNDTSVLPSC 1117

Subject: 938 YNTSNVDEYVRSLPFLNLIGQVLY  
Query: 241 STIAEMCDHPDYARLVDIPSNNKYELNLIVSLPA 274  
STIAEMCDHPDYARLVDIPSNNKYELNLIVSLPA  
Subject: 1118 STIAEMCDHPDYARLVDIPSNNKYELNLIVSLPA 1219

>gi|1273716|gb|AF050215.1|AF050215 Candida albicans chromosome 3 map between CDR1 and DYN1 strain  
HOG759  
Length = 6980

Score = 549 bits (1415), Expect = e-154  
Identities = 272/274 (99%), Positives = 272/274 (99%)  
Frame = +1

Query: 1 MSSAQNDDNBEQVMESVDQANAI SKVDEHIKARFNMLFIKFNLDLPKLAVGNQKSVQKWE 60  
MSSAKNDDNBEQVMESVDQANAI SKVDEHIKARFNMLFIKFNLDLPKLAVGNQKSVQKWE  
Subject: 604 MSSAKNDDNBEQVMESVDQANAI SKVDEHIKARFNMLFIKFNLDLPKLAVGNQKSVQKWE 783

Query: 61 EFKYFHVAYPDVLEFLLDYNEKDKFKVKKVEGIYFTGWCLQMCLOSIFDRPRLIMISKLP 120  
EFKYFHVAYPDVLEFLLDYNEKDKFKVKKVEGIYFTGWCLQMCLOSIFDRPRLIMISKLP  
Subject: 784 EFKYFHVAYPDVLEFLLDYNEKDKFKVKKVEGIYFTGWCLQMCLOSIFDRPRLIMISKLP 963

Query: 121 KHLQKEANLIKAAYDAVTKSKDYTTITSKILSKFVNVEHELVCYNLPYLQVEKLEBIL 180  
KHLQKEANLIKAAYDAVTKSKDYTTITSKIL KFNVEHELVCYNLPYLQVEKLEBIL  
Subject: 964 KHLQKEANLIKAAYDAVTKSKDYTTITSKILKFNVEHELVCYNLPYLQVEKLEBIL 1143

Query: 181 YNTSNVDEYVRSLPFLNLIGQVLYFNHVKKSEALSFLNLIHASYYSKWIQADNDTSVLPSC 240  
YNTSNVDEYVRSLPFLNLIGQVLYFNHVKKSEALSFLNLIHASYYSKWIQADNDTSVLPSC  
Subject: 1144 YNTSNVDEYVRSLPFLNLIGQVLYFNHVKKSEALSFLNLIHASYYSKWIQADNDTSVLPSC 1323

Query: 241 STIAEMCDHPDYARLVDIPSNNKYELNLIVSLPA 274  
STIAEMCDHPDYARLVDIPSNNKYELNLIVSLPA  
Subject: 1324 STIAEMCDHPDYARLVDIPSNNKYELNLIVSLPA 1425

>gi|13356236|gb|U22631.2| Caenorhabditis elegans cosmid F47D12, complete sequence  
Length = 42275

Score = 40.0 bits (92), Expect = 0.30  
Identities = 24/80 (30%), Positives = 36/80 (45%), Gaps = 4/80 (5%)  
Frame = -1

Query: 175 KLEBILYNTSNVDEYVRSLP----NLIGQVLYFNHVKKSEALSFLNLIHASYYSKWQA 230  
K I N + +D S+P NL + YFNH+ K + + IM S+Y WI  
Subject: 18740 KKNISINIDSKLDMIWCSIPLNSENLYCCIRYFNHPIKIRSTGCW--IHKSPYLNWIHF 18567

Query: 231 DNDTSVLPSCSTIAEMCDH 250  
+ V P T+ ++ DH  
Subject: 18566 STNKKVKPCVLTVERQLVDH 18507

>gi|17553483|ref|NM\_065980.1| L Caenorhabditis elegans  
Length = 423

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Identities = 24/80 (30%), Positives = 36/80 (45%), Gaps = 4/80 (5%)  
Frame = -1

Query: 175 KLEBILYNTSNVDEYVRSLP----NLIGQVLYFNHVKKSEALSFLNLIHASYYSKWQA 230  
K I N + +D S+P NL + YFNH+ K + + IM S+Y WI  
Subject: 224 KKNISINIDSKLDMIWCSIPLNSENLYCCIRYFNHPIKIRSTGCW--IHKSPYLNWIHF 61

Query: 231 DNDTSVLPSCSTIAEMCDH 250  
+ V P T+ ++ DH  
Subject: 60 STNKKVKPCVLTVERQLVDH 1

>gi|20197371|gb|AC006387.3| Arabidopsis thaliana chromosome 2 clone T3E17 map CIC02E07, complete  
sequence  
Length = 110149

Score = 32.0 bits (71), Expect(2) = 4.1  
Identities = 25/120 (20%), Positives = 60/120 (49%), Gaps = 4/120 (3%)  
Frame = +3

Query: 114 IMISKLPKHLQKEANLIKAAYDAVTKSKDYTTITSKILSKFVNVEHELVCYNLPYLSQVE 173  
I++ L K L K ++ Y + +S+ T T++S +V++ ++ + +S ++  
Subject: 48288 ILMQLLVKGL-KLTMVATYI-RYQSRISITTEVTSTWVLLR\*VLCKSPISISYK 48464

Query: 174 EKLEBILYNTSNVDEYVRSLPFLNLIGQVLYFNHVKKSEALSFLNLIHASYYSK----WQ 229  
E ++ + + N+ + + + +V Y N++ A + LN+ S YS+ W+Q  
Subject: 48465 EVIQLV--SGNIDQKRMGCISECRKVSXQNNIS\*BEAFDVLLNVLMSIYGRIPGHVWQ 48535

Score = 22.7 bits (47), Expect(2) = 4.1  
Identities = 7/17 (41%), Positives = 12/17 (70%)  
Frame = +1

Query: 233 DTSVLPSCSTIAEMCD 249  
D+ +L SC+T+ +CD  
Subject: 48715 DSRILVSCNTLYSRLCD 48765

Received Time 30. Apr. 18:38 <http://www.ncbi.nlm.nih.gov/blast/Blast.cgi>

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RID=1020140023-011450-20002.

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Rattus norvegicus mRNA for aminopeptidase-B. complete cds

>gi|1754514|db|p87515.1|p87515  
Length = 2192Score = 35.0 bits (79). Expect = 9.7  
Identities = 21/55 (38%), Positives = 30/55 (54%), Gaps = 5/55 (9%)  
Frame = +3Query: 49 VGNQKSVDK---WNEEFKYFHVAYPDVLEFLDYNNPKDKFK-VKKVGGIYFTGW 98  
VG+Q+ DK + +EFK+ + D LEP L+Y P+ K K V + G F W  
Sbjct: 1284 VGDQEQFDKFLKAYVDEPKFQSILAEDEFLEFYLEYFPELKKKGVDSTPGFEFNRW 1448>gi|13592046|ref|NM\_031097.1| Rattus norvegicus aminopeptidase B (Rnpep), mRNA  
Length = 2208Score = 35.0 bits (79). Expect = 9.7  
Identities = 21/55 (38%), Positives = 30/55 (54%), Gaps = 5/55 (9%)  
Frame = +3Query: 49 VGNQKSVDK---WNEEFKYFHVAYPDVLEFLDYNNPKDKFK-VKKVGGIYFTGW 98  
VG+Q+ DK + +EFK+ + D LEP L+Y P+ K K V + G F W  
Sbjct: 1287 VGDQEQFDKFLKAYVDEPKFQSILAEDEFLEFYLEYFPELKKKGVDSTPGFEFNRW 1451>gi|2039142|gb|U61696.1|RN051596 Rattus norvegicus aminopeptidase B mRNA, complete cds  
Length = 2208Score = 35.0 bits (79). Expect = 9.7  
Identities = 21/55 (38%), Positives = 30/55 (54%), Gaps = 5/55 (9%)  
Frame = +3Query: 49 VGNQKSVDK---WNEEFKYFHVAYPDVLEFLDYNNPKDKFK-VKKVGGIYFTGW 98  
VG+Q+ DK + +EFK+ + D LEP L+Y P+ K K V + G F W  
Sbjct: 1287 VGDQEQFDKFLKAYVDEPKFQSILAEDEFLEFYLEYFPELKKKGVDSTPGFEFNRW 1451Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,  
or phase 0, 1 or 2 HTGS sequences)  
Posted date: Apr 29, 2002 1:59 AM  
Number of letters in database: 1,132,994,982  
Number of sequences in database: 1,218,445Lambda K H  
0.317 0.134 0.368Gapped  
Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1,648,687,762

Number of Sequences: 1218445

Number of extensions: 24413213

Number of successful extensions: 103318

Number of sequences better than 10.0: 16

Number of HSP's better than 10.0 without gapping: 38293

Number of HSP's successfully gapped in prelim test: 5836

Number of HSP's that attempted gapping in prelim test: 52250

Number of HSP's gapped (non-prelim): 69771

length of query: 324

length of database: 1,809,320,759

effective HSP length: 136

effective length of query: 188

effective length of database: 1,643,612,239

effective search space: 308999100932

effective search space used: 308999100932

frameshift window, decay const: 50, 0.1

T: 13

A: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 79 (35.0 bits)

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Wednesday, 30 April 2002

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Nucleotide



Search Nucleotide for

Limits

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History

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Related Sequences, Protein, Taxonomy

1: AF050215. Candida albicans ...[gi:3273716]

LOCUS AF050215 6980 bp DNA linear PLN 01-JUL-1998  
DEFINITION Candida albicans Tsa2 retrotransposon gag polyprotein (gag) and pol polyprotein (pol) genes, complete cds.  
ACCESSION AF050215  
VERSION AF050215.1 GI:3273716  
KEYWORDS  
SOURCE Candida albicans.  
ORGANISM Candida albicans  
Bukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;  
Saccharomycetales; mitosporic Saccharomycetales; Candida.  
REFERENCE 1 (bases 1 to 6980)  
AUTHORS Goodwin, T.J.D. and Poulter, R.T.M.  
TITLE Temperature- and strain-dependent expression of the pCal  
retrotransposon of Candida albicans  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 6980)  
AUTHORS Goodwin, T.J.D. and Poulter, R.T.M.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-1998) Department of Biochemistry, University of  
Otago, Cumberland Street, Dunedin, New Zealand  
FEATURES  
Location/Qualifiers  
source 1..6980  
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/strain="huc759"  
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LTR 207..486  
/note="5' long terminal repeat"  
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/note="complements cRNA Arg(UCU) fragment"  
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CLQSIFDRFLIMISKLPKHLQKLANLIKAAVDAVTKSKDYTTISKILSKFVNVHEL  
VVCYNLPLYLSQVEKLEELLYNTSNVDEYVRSPLNLIQGVLYFNHVKRSRLSLFLN  
IHASYSKWIQADNDTSULPSCSTIABNCHDFDYARLVDFENKVELNLIVSLPABE  
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/note="potentially suppressed stop codon"  
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/gene="pol"  
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transcriptase, RNase H"  
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/db\_xref="GI:3273718"  
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PSEESLECDPDDVGLADMLSNAGDDKDKSKMNMSEYQEHVSSRALINSLTEVDL  
DVRISPYGVEQLLPTGDKNDIYNFHLMSNMISTEKILLCKYGGVLHTSKESLQKIA  
DCKVCLLSNAKQSHHSHSRKASRHERLHCDTIGFSENNKWLTSVIDENTGYT  
EGYITKQKVKOLLIQELKTNKPNKVKVAYFRSDNABFPQPSDLAEFGIWRETIA  
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TVSEDMHTSDYFETSAEPEQNPPLSANQKRVTERIDEGENISPPGGDDSVVINSV  
EQSNVETEDAGNSPIQDQVSQGRILNEQTIDVQVAKVIRNEKISFINSLLDHTELA  
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Received Time 30 Apr 18:38 nbez/query.fg?cmd=Fetch&amp;db=nucleotide&amp;file\_id=3273716&amp;seq=

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CDPREAIRVINTOETKFO.U BIOCHEMISTRY:SPYVTRSGRTV.DNFRYLHA  
VVKRIDYNDPQWIKSMNANLAKKALVIAOVSIVKPIKMGVHTKIDSLKGVV  
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ASITHSNPIYVFPKSVPLKQTHCWLKNSVVLKQSQFQWHTTKRVLDIGENOV  
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GTEFKATBEGSYTYLQYVDDILMVSSQKVIDNFVDOLRDHPFVKVGTISNYL  
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NLVQWAKKQTVTAQSSAACEMALNYTMLKATIKNTMDLGEVVGKINCHODNOAV  
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VEGHIKRLDLKDNQTSIONATAS

misc feature

1579..1586

/gene="pol"

/note="purine-rich tract"

misc feature

1587..1661

/gene="pol"

/note="encodes putative pseudocodon"

misc feature

3661..3671

/gene="pol"

/note="polypurine tract 2"

misc feature

6342..6352

/note="polypurine tract 1"

LWR

6353..6632

/note="3' long terminal repeat"

misc feature

6633..6637

/note="3' target site duplication"

BASE COUNT

2447 A

1121 C

1338 G

2074 T

ORIGIN

1 aataaaccat ccaattgttt ctaactccaa aacccgccaa acaagccccc tataaagacc  
61 aatcagctat tctggcgc cgcacaccag cgcacaccag cgcacaccag cgcacaccag  
121 aatcagctat tctggcgc cgcacaccag cgcacaccag cgcacaccag cgcacaccag  
181 aataaaccat ccaattgttt ctaactccaa aacccgccaa acaagccccc tataaagacc  
241 aatcagctat tctggcgc cgcacaccag cgcacaccag cgcacaccag cgcacaccag  
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Revised: October 24, 2001.

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